

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/322,021

DATE: 07/30/1999  
TIME: 14:41:24

INPUT SET: S32704.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: ARMITAGE, RICHARD  
6 FANSLOW, WILLIAM  
7 SPRIGGS, MELANIE  
8 SRINIVASAN, SUBHASHINI  
9 GIBSON, MARYLOU  
10  
11 (ii) TITLE OF INVENTION: NOVEL CYTOKINE  
12  
13 (iii) NUMBER OF SEQUENCES: 23  
14  
15 (iv) CORRESPONDENCE ADDRESS:  
16 (A) ADDRESSEE: IMMUNEX CORPORATION  
17 (B) STREET: 51 UNIVERSITY STREET  
18 (C) CITY: SEATTLE  
19 (D) STATE: WASHINGTON  
20 (E) COUNTRY: USA  
21 (F) ZIP: 98101  
22  
23 (v) COMPUTER READABLE FORM:  
24 (A) MEDIUM TYPE: Floppy disk  
25 (B) COMPUTER: Apple Macintosh  
26 (C) OPERATING SYSTEM: Apple Operating System 7.1  
27 (D) SOFTWARE: Microsoft Word for Apple, version 5.1a  
28  
29 (vi) CURRENT APPLICATION DATA:  
30 (A) APPLICATION NUMBER: 09/322,021  
31 (B) FILING DATE:  
32 (C) CLASSIFICATION:  
33  
34 (vii) PRIOR APPLICATION DATA:  
35 (A) APPLICATION NUMBER: 08/249,189  
36 (B) FILING DATE:  
37 (C) CLASSIFICATION:  
38  
39 (vii) PRIOR APPLICATION DATA:  
40 (A) APPLICATION NUMBER: 07/805,723  
41 (B) FILING DATE: December 5, 1991  
42 (C) CLASSIFICATION: 514  
43  
44 (vii) PRIOR APPLICATION DATA:  
45 (A) APPLICATION NUMBER: 07/783,707  
46 (B) FILING DATE: October 25, 1991

ENTERED

-->dc

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--> 47 (C) CLASSIFICATION: 514  
48  
49 (viii) ATTORNEY/AGENT INFORMATION:  
50 (A) NAME: Perkins, Patricia A.  
51 (B) REGISTRATION NUMBER: 34,693  
52 (C) REFERENCE/DOCKET NUMBER: 2802-C  
53  
54 (ix) TELECOMMUNICATION INFORMATION:  
55 (A) TELEPHONE: 2065870430  
56 (B) TELEFAX: 2065870606  
57  
58  
59 (2) INFORMATION FOR SEQ ID NO:1:  
60  
61 (i) SEQUENCE CHARACTERISTICS:  
62 (A) LENGTH: 783 base pairs  
63 (B) TYPE: nucleic acid  
64 (C) STRANDEDNESS: single  
65 (D) TOPOLOGY: linear  
66  
67 (ii) MOLECULE TYPE: cDNA  
68  
69 (iii) HYPOTHETICAL: NO  
70  
71 (iv) ANTI-SENSE: NO  
72  
73 (vi) ORIGINAL SOURCE:  
74 (A) ORGANISM: MOUSE  
75  
76 (vii) IMMEDIATE SOURCE:  
77 (B) CLONE: CD40-L  
78  
79 (ix) FEATURE:  
80 (A) NAME/KEY: CDS  
81 (B) LOCATION: 1..783  
82  
83  
84 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
85  
86 ATG ATA GAA ACA TAC AGC CAA CCT TCC CCC AGA TCC GTG GCA ACT GGA 48  
87 Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly  
88 1 5 10 15  
89  
90 CTT CCA GCG AGC ATG AAG ATT TTT ATG TAT TTA CTT ACT GTT TTC CTT 96  
91 Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu  
92 20 25 30  
93  
94 ATC ACC CAA ATG ATT GGA TCT GTG CTT TTT GCT GTG TAT CTT CAT AGA 144  
95 Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg  
96 35 40 45  
97  
98 AGA TTG GAT AAG GTC GAA GAG GAA GTA AAC CTT CAT GAA GAT TTT GTA 192  
99 Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val

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|     |   |     |     |     |
|-----|---|-----|-----|-----|
| 100 | 50  | 55  | 60  |     |
| 101 |   |     |     |     |
| 102 | TTC ATA AAA AAG CTA AAG AGA TGC AAC AAA GGA GAA GGA TCT TTA TCC |     |     | 240 |
| 103 | Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser |     |     |     |
| 104 | 65  | 70  | 75  | 80  |
| 105 |   |     |     |     |
| 106 | TTG CTG AAC TGT GAG GAG ATG AGA AGG CAA TTT GAA GAC CTT GTC AAG |     |     | 288 |
| 107 | Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys |     |     |     |
| 108 |   | 85  | 90  | 95  |
| 109 |   |     |     |     |
| 110 | GAT ATA ACG TTA AAC AAA GAA GAG AAA AAA GAA AAC AGC TTT GAA ATG |     |     | 336 |
| 111 | Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met |     |     |     |
| 112 |   | 100 | 105 | 110 |
| 113 |   |     |     |     |
| 114 | CAA AGA GGT GAT GAG GAT CCT CAA ATT GCA GCA CAC GTT GTA AGC GAA |     |     | 384 |
| 115 | Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu |     |     |     |
| 116 |   | 115 | 120 | 125 |
| 117 |   |     |     |     |
| 118 | GCC AAC AGT AAT GCA GCA TCC GTT CTA CAG TGG GCC AAG AAA GGA TAT |     |     | 432 |
| 119 | Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr |     |     |     |
| 120 |   | 130 | 135 | 140 |
| 121 |   |     |     |     |
| 122 | TAT ACC ATG AAA AGC AAC TTG GTA ATG CTT GAA AAT GGG AAA CAG CTG |     |     | 480 |
| 123 | Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu |     |     |     |
| 124 | 145   | 150 | 155 | 160 |
| 125 |   |     |     |     |
| 126 | ACG GTT AAA AGA GAA GGA CTC TAT TAT GTC TAC ACT CAA GTC ACC TTC |     |     | 528 |
| 127 | Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe |     |     |     |
| 128 |   | 165 | 170 | 175 |
| 129 |   |     |     |     |
| 130 | TGC TCT AAT CGG GAG CCT TCG AGT CAA CGC CCA TTC ATC GTC GGC CTC |     |     | 576 |
| 131 | Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu |     |     |     |
| 132 |   | 180 | 185 | 190 |
| 133 |   |     |     |     |
| 134 | TGG CTG AAG CCC AGC AGT GGA TCT GAG AGA ATC TTA CTC AAG GCG GCA |     |     | 624 |
| 135 | Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala |     |     |     |
| 136 |   | 195 | 200 | 205 |
| 137 |   |     |     |     |
| 138 | AAT ACC CAC AGT TCC TCC CAG CTT TGC GAG CAG CAG TCT GTT CAC TTG |     |     | 672 |
| 139 | Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu |     |     |     |
| 140 |   | 210 | 215 | 220 |
| 141 |   |     |     |     |
| 142 | GGC GGA GTG TTT GAA TTA CAA GCT GGT GCT TCT GTG TTT GTC AAC GTG |     |     | 720 |
| 143 | Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val |     |     |     |
| 144 | 225   | 230 | 235 | 240 |
| 145 |   |     |     |     |
| 146 | ACT GAA GCA AGC CAA GTG ATC CAC AGA GTT GGC TTC TCA TCT TTT GGC |     |     | 768 |
| 147 | Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly |     |     |     |
| 148 |   | 245 | 250 | 255 |
| 149 |   |     |     |     |
| 150 | TTA CTC AAA CTC TGA   |     |     | 783 |
| 151 | Leu Leu Lys Leu   |     |     |     |
| 152 |   | 260 |     |     |

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153

154

155 (2) INFORMATION FOR SEQ ID NO:2:

156

157 (i) SEQUENCE CHARACTERISTICS:

158 (A) LENGTH: 260 amino acids

159 (B) TYPE: amino acid

160 (D) TOPOLOGY: linear

161

162 (ii) MOLECULE TYPE: protein

163

164 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

165

166 Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly  
167 1 5 10 15

168

169 Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu  
170 20 25 30

171

172 Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg  
173 35 40 45

174

175 Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val  
176 50 55 60

177

178 Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser  
179 65 70 75 80

180

181 Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys  
182 85 90 95

183

184 Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met  
185 100 105 110

186

187 Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu  
188 115 120 125

189

190 Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr  
191 130 135 140

192

193 Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu  
194 145 150 155 160

195

196 Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe  
197 165 170 175

198

199 Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu  
200 180 185 190

201

202 Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala  
203 195 200 205

204

205 Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/322,021

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206          210          215          220
207
208 Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val
209 225          230          235          240
210
211 Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly
212          245          250          255
213
214 Leu Leu Lys Leu
215          260
216
217

```

## (2) INFORMATION FOR SEQ ID NO:3:

```

220 (i) SEQUENCE CHARACTERISTICS:
221 (A) LENGTH: 740 base pairs
222 (B) TYPE: nucleic acid
223 (C) STRANDEDNESS: single
224 (D) TOPOLOGY: linear

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225
226 (ii) MOLECULE TYPE: cDNA

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227
228 (iii) HYPOTHETICAL: NO

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229
230 (iv) ANTI-SENSE: NO

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231
232 (vi) ORIGINAL SOURCE:
233 (A) ORGANISM: HUMAN

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234
235 (vii) IMMEDIATE SOURCE:
236 (B) CLONE: IgG1 Fc

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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240
241 CGGTACCGCT AGCGTCGACA GGCCTAGGAT ATCGATACGT AGAGCCCAGA TCTTGTGACA      60
242
243 AAACCTCACAC ATGCCACCG TGCCAGCAC CTGAACTCCT GGGGGGACCG TCAGTCTTCC      120
244
245 TCTTCCCCCCC AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG GTCACATGCG      180
246
247 TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT CAACTGGTAC GTGGACGGCG      240
248
249 TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA GTACAACAGC ACGTACCGGG      300
250
251 TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAGGAC TACAAGTGCA      360
252
253 AGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TGCAGAAAAC CATCTCCAAA GCCAAAGGGC      420
254
255 AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCCATCCCG GGATGAGCTG ACCAAGAACC      480
256
257 AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTATCCCAG GCACATCGCC GTGGAGTGGG      540
258

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/322,021**

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| Line | Error                | Original Text          |
|------|----------------------|------------------------|
| 42   | Wrong Classification | (C) CLASSIFICATION:514 |
| 47   | Wrong Classification | (C) CLASSIFICATION:514 |